Variable Heavy

```
A4.6.1     EIQLVQSGPELKQPGETVRISCKASGYTFTNYGMNWVKQAPGKGLKWMG
              *     *   *: *     *** *   *                     *         * *
F(ab)-12   EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWVG
                                          *   ** *  *                          *
humIII     EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS
           1        10        20        30        40
```

```
A4.6.1     WINTYTGEPTYAADFKRRFTFSLETSASTAYLQISNLKNDDTATYFCAK
                           *   *      *** ***       * *
F(ab)-12   WINTYTGEPTYAADFKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAK          Fig. 1A
              *  ****  ***    *** *    *  *   *   *                       *
humIII     VISGDGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
           50  a        60        70        80  abc      90
```

```
A4.6.1     YPHYYGSSHWYFDVWGAGTTVTVSS (SEQ ID NO:9)
                        *   *
F(ab)-12   YPHYYGSSHWYFDVWGQGTLVTVSS (SEQ ID NO:7)
              *              *
humIII     G----------FDYWGQGTLVTVSS (SEQ ID NO:11)
                            110
```

Variable Light

```
A4.6.1     DIQMTQTTSSLSASLGDRVIISCSASQDISNYLNWYQQKPDGTVKVLIY
                    **            *         * *                      ****
F(ab)-12   DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIY
                                            *      *        *             *
humKI      DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIY
           1        10        20        30        40
```

Fig. 1B

```
A4.6.1     FTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYSTVPWTF
                              **        * *    *
F(ab)-12   FTSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTF
              **    *                                            ***
humKI      AASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTF
           50        60        70        80        90
```

```
A4.6.1     GGGTKLEIKR (SEQ ID NO:10)
              *   *
F(ab)-12   GQGTKVEIKR (SEQ ID NO:8)

humKI      GQGTKVEIKR (SEQ ID NO:12)
           100
```

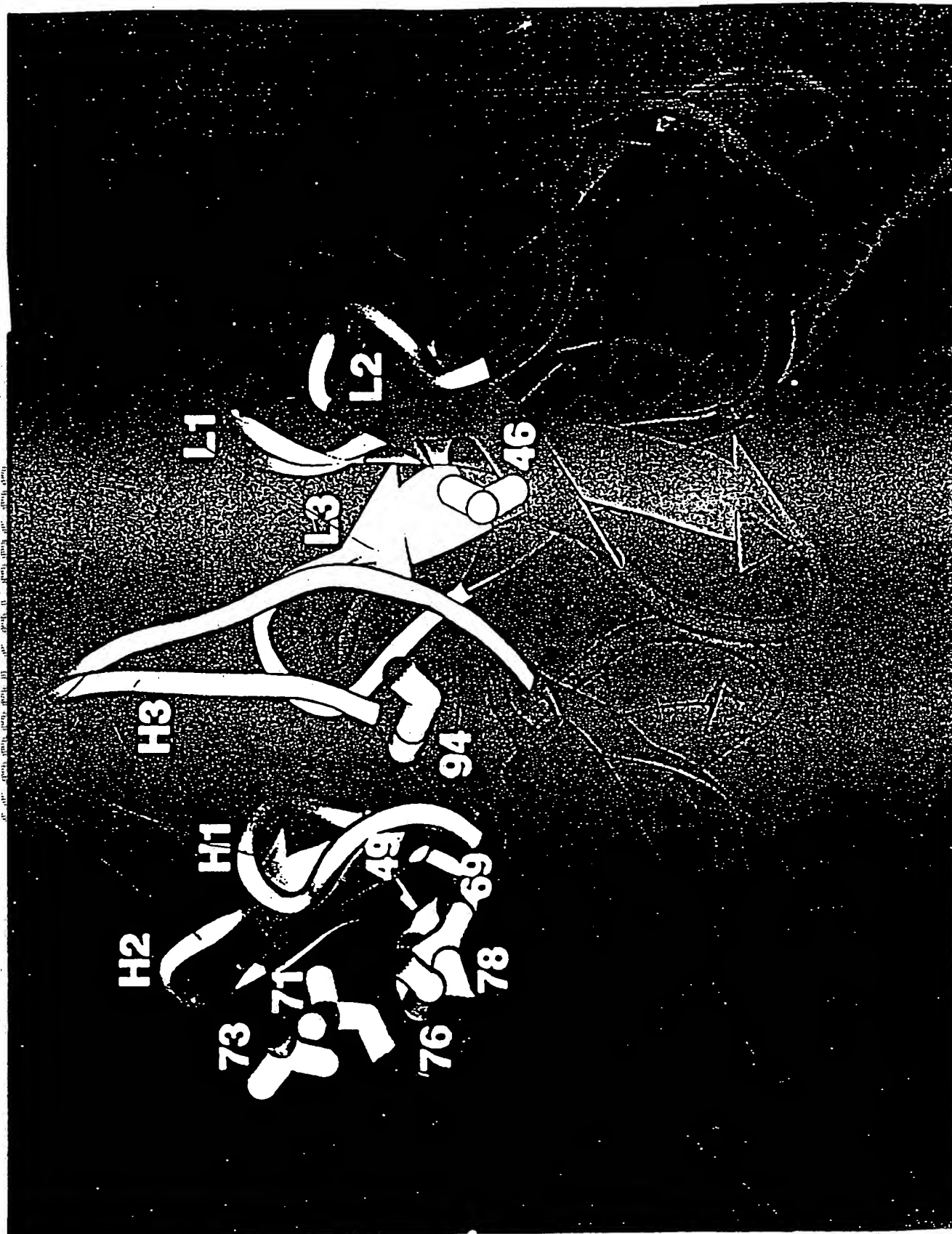Fig. 2

Fig. 3

Fig. 4

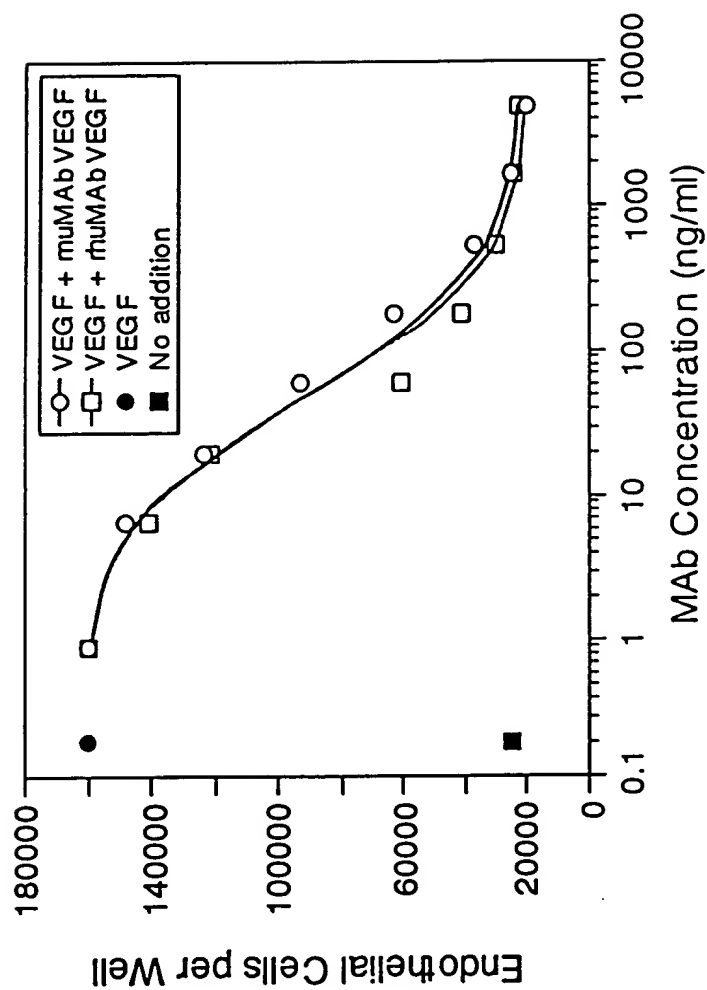## V_L domain
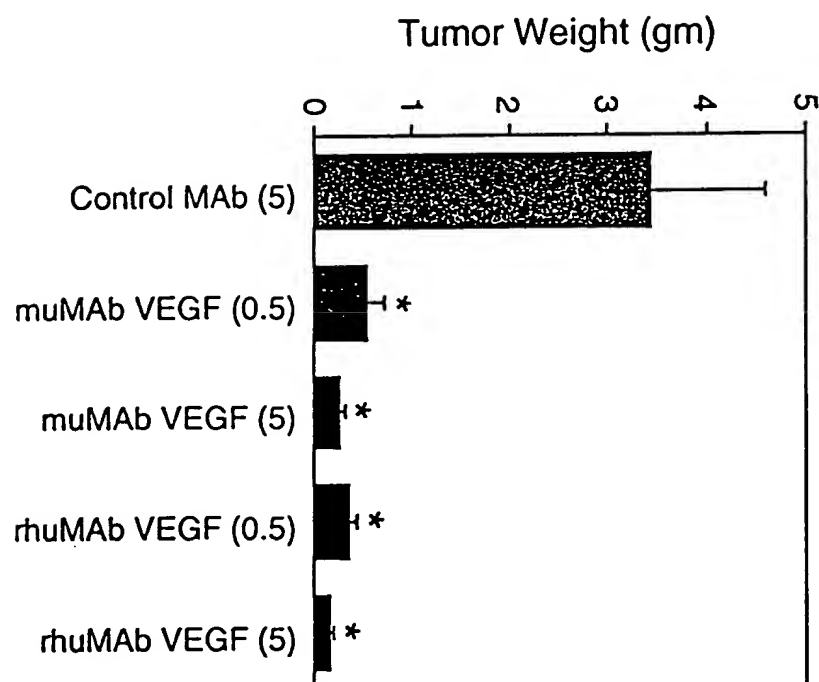
```
              10         20         30         40
A4.6.1  DIQMTQTTSSLSASLGDRVIISCSASQDISNYLNWYQQKP
          **        *       *  *
hu2.0   DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKP

hu2.10  DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKP
```

```
              50         60         70         80
A4.6.1  DGTVKVLIYFTSSLHSGVPSRFSGSGSGTDYSLTISNIEP
        ****  *                          **   * *
hu2.0   GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQP
                                              .
hu2.10  GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDYTLTISSLQP
```

```
              90        100 .
A4.6.1  EDIATYYCQQYSTVPWTFGGGTKLEIK (SEQ ID NO:10)
          *                 *   *
hu2.0   EDFATYYCQQYSTVPWTFGQGTKVEIK (SEQ ID NO:13)

hu2.10  EDFATYYCQQYSTVPWTFGQGTKVEIK (SEQ ID NO:15)
```

– V_H domain

```
              10         20         30         40
A4.6.1  EIQLVQSGPELKQPGETVRISCKASGYTFTNYGMNWVKQA
         *    *  ** *   *** * *                *
hu2.0   EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQA
                                             .
hu2.10  EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWIRQA
```

```
           50 a        60         70         80
A4.6.1  PGKGLKWMGWINTYTGEPTYAADFKRRFTFSLETSASTAYL
         * *                        * *** ** *
hu2.0   PGKGLEWVGWINTYTGEPTYAADFKRRFTISRDNSKNTLYL
                                      . . .. .
hu2.10  PGKGLEWVGWINTYTGEPTYAADFKRRFTISLDTSASTVYL
```

```
          abc      90       100abcdef      110
A4.6.1  QISNLKNDDTATYFCAKYPHYYGSSHWYFDVWGAGTTVTVSS (SEQ ID NO:9)
        *** ***   * *  *                       * *
hu2.0   QMNSLRAEDTAVYYCARYPHYYGSSHWYFDVWGQGTLVTVSS (SEQ ID NO:14)
                          .
hu2.10  QMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTLVTVSS (SEQ ID NO:16)
```
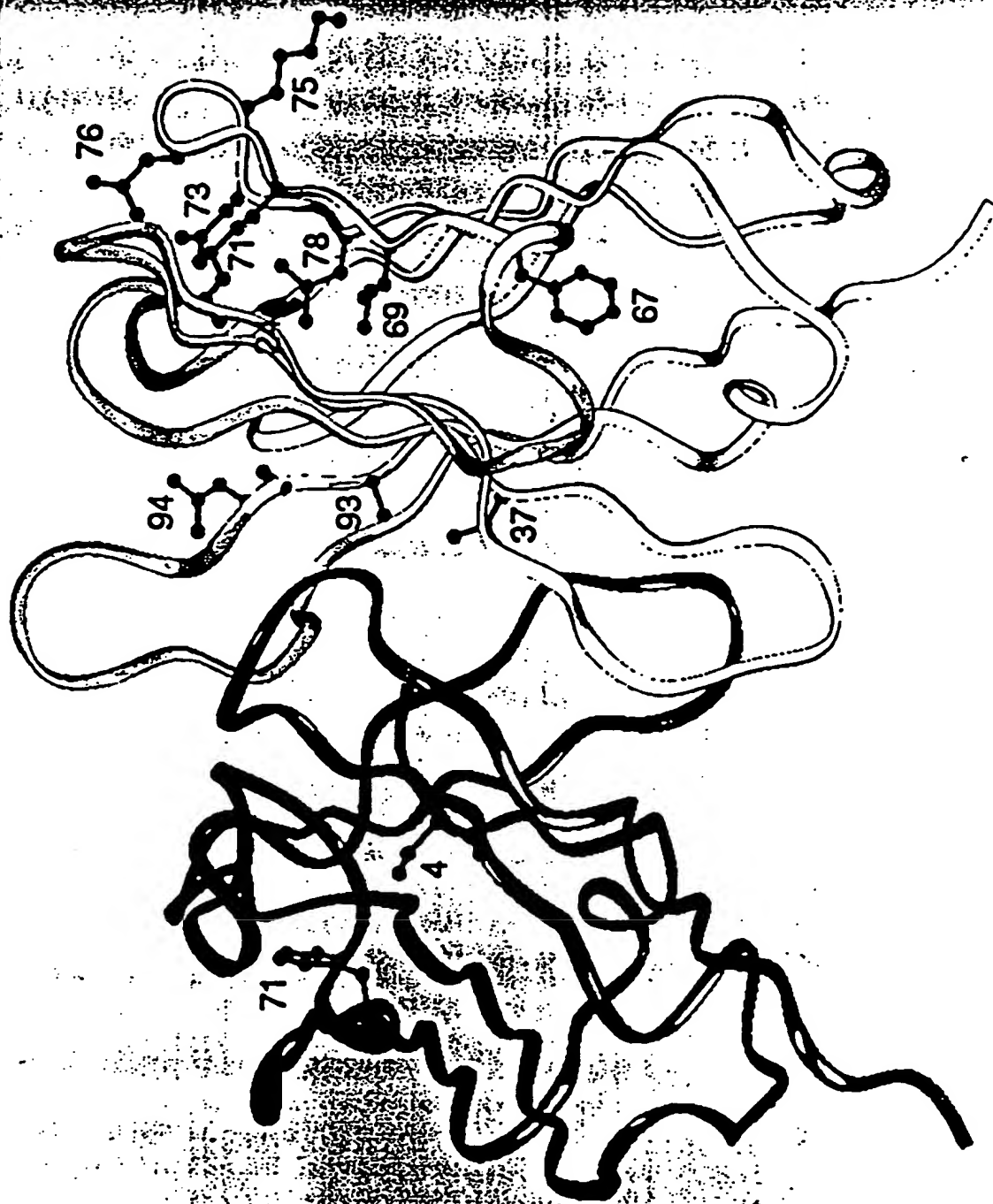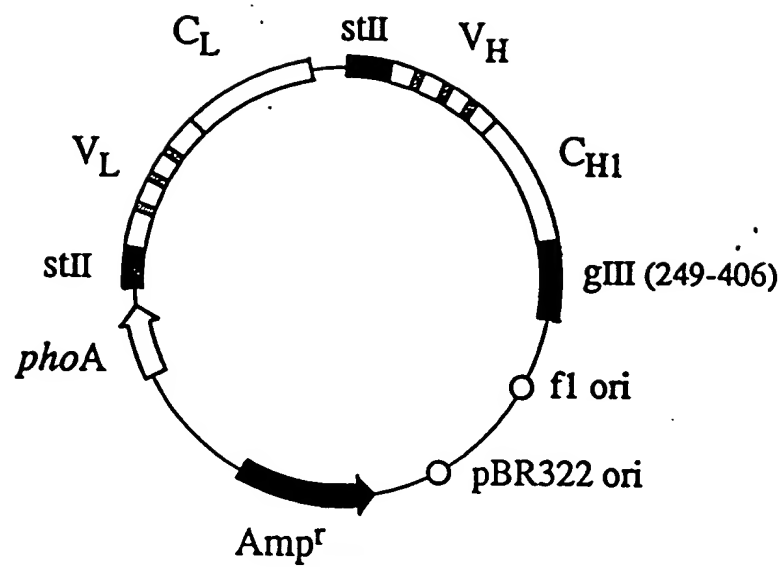
75

76

73
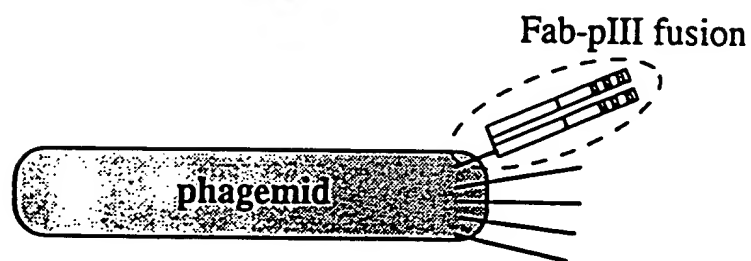
71

78

69

67

94

93

37

4

71

Fig. 6

Fig. 7

```
1    GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTTTGA GATTATCGTC ACTGCAATGC
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAAAACT CTAATAGCAG TGACGTTACG

101  TTCGCAATAT GGGCGCAAAT GACCAACAGC GGTTGATTGA TCAGGTAGAG GGGGCGCTGT ACGAGGTAAA GCCATTCCTG ACGACGATAC
     AAGCGTTATA CCGCGTTTTA CTGGTTGTCG CCAACTAACT AGTCCATCTC CCCCGCGACA TGCTCCATTT CGGCGCTACG TGCTGCTATG

201  GGAGCTGCTG CGGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT AAAAAGTTAA TCTTTCAAC AGCTGTCATA AGTTGTCAC GGCCGAGACT
     CCTCGACGAC GGCGCTAATGC ATTTCTTCAA TAACTTCGTA GGAGCAGTCA TTTTTCAATT AGAAAAGTTG TCGACAGTAT TCAACAGTG CCGGCTCTGA

301  TATAGTCGCT TGTTTTTAT ATTTGTAACT AGAATTCGAG GGGGATCCTC TAGAGGTTGA GGTGATTTA TGAAAAAGAA
     ATATCAGCGA AACAAAAATA TAAACATTGA TCTTAAGCTC CCCCTAGGAG ATCTCCAACT CCACTAAAAT ACTTTTTCTT
                                                                              M etLysLysAsn

                                                          Begin stII signal sequence
401  TATCGCATTT CTTCTTGCAT CTATGTTCGT TTTTTCTATT GCTACAAACG TATCCAGTTG ACCCAGTCCC CGAGCTCCCT GTCCGCCTCT
     ATAGCGTAAA GAAGAACGTA GATACAAGCA AAAAAGATAA CGATGTTTGC ATAGGTCAAC TGGGTCAGGG GCTCGAGGGA CAGGCGGAGA
-19  IleAlaPhe LeuLeuAlaS erMetPheVa laTyrAlaAs plleGlnLeu ThrGlnSerP roSerSerLe uSerAlaSer

                                                          Begin light chain
501  GTGGGCGATA GGGTCACCAT CACCTGCAGC GCAAGTCAGG ATATTAGCAA CTATTTAAAC TGGTATCAAC AGAAAACCAGG AAAAGCTCCG AAACTACTGA
     CACCCGCTAT CCCAGTGGTA GTGGACGTCG CGTTCAGTCC TATAATCGTT GATAAATTTG ACCATAGTTG TCTTTTGGTCC TTTTCGAGGC TTTGATGACT
15   ValGlyAspA rgValThrIl eThrCysSer AlaSerGlnA spIleSerAs nTyrLeuAsn TrpTyrGlnG lnLysProGl yLysLeuLeuIle

601  TTTACTTCAC CTCCTCTCTC CACTCTGGAG TCCCTTCTCG CTTCTCTGGA TCCGGTTCTG GGACGGATTA CACTCTGACC ATCAGCAGTC TGCAGCCAGA
     AAATGAAGTG GAGGAGAGAG GTGAGACCTC AGGGAAGAGC GAAGAGACCT AGGCCAAGAC CCTGCCTAAT GTGAGACTGG TAGTCGTCAG ACGTCGGTCT
49   TyrPheTh rSerSerLeu HisSerGlyV alProSerAr gPheSerGly SerGlySerG lyThrAspTy rThrLeuThr IleSerSerL euGlnProGlu

701  AGACTTCGCA ACTTATTACT GTCAACAGTA TAGCACCGTG CCGTGGACGT TTGGACAGGG TACCAAGGTG GAGATCAAAC GAACTGTGGC TGCACCATCT
     TCTGAAGCGT TGAATAATGA CAGTTGTCAT ATCGTGGCAC GGCACCTGCA AACCTGTCCC ATGGTTCCAC CTCTAGTTTG CTTGACACCG ACGTGGTAGA
82   AspPheAla ThrTyrTyrC ysGlnGlnTy rSerThrVal ProTrpThrP heGlyGlnGl yThrLysVal GluIleLysA rgThrValAl aAlaProSer

801  GTCTTCATCT TCCCGCCATC TGATGAGCAG TTGAAATCTG GAACTGCTTC TGTTGTGTGC CTGCTGAATA ACTTCTATCC CAGAGAGGCC AAAGTACAGT
     CAGAAGTAGA AGGGCGGTAG ACTACTCGTC AACTTTAGAC CTTGACGAAG ACAACACACG GACGACTTAT TGAAGATAGG GTCTCTCCGG TTTCATGTCA
115  ValPheIleP heProProSe rAspGluGln LeuLysSerG lyThrAlaSe rValValCys LeuLeuAsnA snPheTyrPr oArgGluAla LysValGlnTrp

901  GGAAGGTGGA TAACGCCCTC CAATCGGGTA ACTCCCAGGA GAGTGTCACA GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA CCCTGACGCT
     CCTTCCACCT ATTGCGGGAG GTTAGCCCAT TGAGGGTCCT CTCACAGTGT CTCGTCCTGT CGTTCCTGTC GTGGATGTCG GAGTCGTCGT GGGACTGCGA
149  LysValAs pAsnAlaLeu GlnSerGlyN snSerGlnGl uSerValThr GluGlnAspS erLysAspSe rThrTyrSer LeuSerSerT hrLeuThrLeu

1001 GAGCAAAGCA GACTACGAGA AACACAAAGT CTACGCCTGC GAAGTCACCC ATCAGGGCCT GAGCTCGCCC GTCACAAAGA GCTTCAACAG GGGAGAGTGT
     CTCGTTTCGT CTGATGCTCT TTGTGTTTCA GATGCGGACG CTTCAGTGGG TAGTCCCGGA CTCGAGCGGG CAGTGTTTCT CGAAGTTGTC CCCTCTCACA
182  SerLysAla AspTyrGluL ysHisLysVa lTyrAlaCys GluValThrH lsGlnGlyLe uSerSerPro ValThrLysS erPheAsnAr gGlyGluCys
```

Fig. 8A

```
1101  TAAGCTGATC CTCTACGCCG GACCGCATCGT GGCCCTAGTA CGCAACTAGT CGTAAAAAGG GTAATCTAGAG GTTGAGGTGA TTTTATGAAA AAGAATATCG
      ATTCGACTAG GAGATGCGGC CTGGCTAGCA CCGGGATCAT GCGGTTGATCA CATAGATCTC CAACTCCACT AAAATACTTT TTCTTATAGC
215   OC*           Begin stII signal sequence                                                  -23 MetLys LysAsnIleAla

1201  CATTCTCTCT TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGGCTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT AGCCAGGGGG
      GTAAGAGAGA ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCCGATG CGACTCCAAG TCGACCACCT CAGACCGCCA TCGGTCCCCC
-17   PheLeuLeu uAlaSerMet PheValPhes erIleAlaTh rAsnAlaTyr AlaGluValG lnLeuValGl uSerGlyGly lnProGlyGly
                         Begin heavy chain

1301  CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG GTATGAACTG GTATCCGTCAG GCCCCGGGTA ATGGGTTGGA
      GAGTGAGGCA AACAGGACAC GTCGAAGACC GATATGGAAG TGGTTGATAC CATACTTGAC CATAGGCAGTC CGGGGCCCAT TACCCAACCT
17    SerLeuArg LeuSerCysA laAlaSerGl yTyrThrPhe ThrAsnTyrG lyMetAsnTr pIleArgGln AlaProGlyL ysGlyLeuGl uTrpValGly

1401  TGGATTAACA CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTTACT ATATCTGCAG ACACCTCCAG CAACACAGTT TACCTGCAGA
      ACCTAATTGT GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAAAATGA TATAGACGTC TGTGGAGGTC GTTGTGTCAA ATGGACGTCT
50    TrpIleAsnT hrTyrThrGl yGluProThr TyrAlaAlaA spPheLysAr gArgPheThr IleSerAlaA spThrSerSe rAsnThrVal TyrLeuGlnMet

1501  TGAACAGCCT GCGCGCTGAG GACACTGCCG TCTATTACTG CGCCACTATT ATGGGAGCAG TTCGACGTCT GGGGTCAAGG
      ACTTGTCGGA CGCGCGACTC CTGTGACGGC AGATAATGAC GGCGTGATAA TACCCTCGTC AAGCTGCAGA CCCCAGTTCC
84    AsnSerLe uArgAlaGlu AspThrAlaV alTyrTyrCy sAlaThrIle MetGlyAlaV alArgArgLeu rPheAspValT rpGlyGlnGly

1601  AACCCTGGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC AGCACCTCTG GGGGCACAGC GGCCCTGGGC
      TTGGGACCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGGT AGCCAGAAGG GGGACCGTGG TCGTGGAGAC CCCCGTGTCG CCGGGACCCG
117   ThrLeuVal ThrValSerS erAlaSerTh rLysGlyPro SerValPheP roLeuAlaPr oSerThrSerG lyGlyThrAl aAlaLeuGly

1701  TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC CCCGGCTGTC CTACAGTCCT CCCGGCTGTC CTACAGTCCT
      ACGGACCAGT TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG GGGCCGACAG GATGTCAGGA GGGCCGACAG GATGTCAGGA
150   CysLeuValL ysAspTyrPh eProGluPro ValThrValS erTrpAsnSe rGlyAlaLeu ThrSerGlyV alHisThrPh eProAlaVal LeuGlnSerSer

1801  CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA
      GTCCTGAGAT GAGGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTTGTGGTT
184   GlyLeuTy rSerLeuSer SerValValT hrValProSe rSerSerLeu GlyThrGlnT hrTyrIleCy sAsnValAsn HisLysPros erAsnThrLys

1901  GGTGGACAAG AAAGTTGAGC CCAAATCTTG TGACAAAACT CACCTCTAGA GTGGCGGTGG CTCTGGTTCC CTCTGGTTCC ATTATGAAAA GATGGCAAAC
      CCACCTGTTC TTTCAACTCG GGTTTAGAAC ACTGTTTTGA GTGGAGATCT CACCGCCACC GAGACCAAGG GAGACCAAGG TAATACTTTT CTACCGTTTG
217   ValAspLys LysValGluP roLysSerCy sAspLysThr HisLeuAM*S aspLysThr HisLeuAM*S erGlyGlyGl yLyGlySer spTyrGluLuy sMetAlaAsn
                                                                 Begin g3p domain
                                                 end light chain

2001  GCTAATAAGG GGGCTATGAC CGAAAAATGCC GATGAAAACG CGCTACAGTC GGCAAACTG ATTCTGTCGC TACTGATTAC GGTGTCGCTA ATGGCTCAAG
      CGATTATTCC CCCGATACTG GCTTTTTACG GCTTTTTGC GCGATGTCAG CCGTTTGAAC TAAGACAGCG ATGACTAATG TACCGAGTTC TACCGTTGAC
250   AlaAsnLysG lyAlaMetTh rGluLysCy sAspGluAsn AlaLeuGlnSe rGlnAsnLeuA laAspAlaLys GlyLysLeuA rAsnSerGln MetAlaGlnV

2101  TCGATGGTTT CATTGGTGAC GTTCCCGGCC TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG
      AGCTACCAAA GTAACCACTG CAAGGGCCGG AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC
284   AspGlyPh eIleGlyAsp ValProGlyL euAlaAsnGl yAsnGlyAla ThrGlyAspP heAlaGlySe rAsnSerGln MetAlaGlnV alGlyAspGly

2201  TGATAAATTCA CCTTTAATGA ATAATATTTA TCAATATTTA CCTTTTGTCT TTAGGGCTGG TAAACCATAT TTAGGGTATA ATTGGTATA
      ACTATTAAGT GGAAATTACT TATTATAAAT AGTTATAAAT GGAAAACAGA GAGTTAGCCA ATTCGCGACC AATCGCATAT TAACCATAT
317   AspAsnSer ProLeuMetA snAsnPheA gGlnTyrLeu ProSerLeuP roPheValP roGlnServa lGluCysArg lGlyAlaGl yLysProTyr
```

Fig. 8B

```
2301 GAATTTTCTA TTGATTGTGA CAAAATAAAC TTATTCCGTG GTTCTTTTGC TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA
     CTTAAAAGAT AACTAACACT GTTTTATTTG AATAAGCAC..CAGAAACC..CAAAGAAAT..ATACAACGAT ACATAAACAT GCAAACGAT
350  GluPheSerI leAspCysAs lePlysIleAsn LeuPheArgG lyValPheAl aPheLeuLeu TyrValAlaT hrPheMetTy rValAlaAsn

2401 ACATACTGCG TAATAAGGAG TCTTAATCAT GCCAGTTCTT TTGGCTAGCG CCGCCCTATA CCTTGTCTGC TGGCGTGCGG TGCATGGAGC
     TGTATGACGC ATTATTCCTC AGAATTAGTA CGGTCAAGAA AACCGATCGC GGCGGGATAT GGAACAGACG ACGGGGCGCA ACGTACCTCG
384  IleLeuAr gAsnLysGlu SerOC* (SEQ ID NO: 100)
     end g3 protein

2501 CGGGCCACCT CGACCTGAAT GGAAGCCGGC GGCACCTCGC TAACGGATTC ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGGAGAA CTGTGAATGC
     GCCCGGTGGA GCTGGACTTA CCTTCGGCCG CCGTGGAGCG ATTGCCTAAG TGGTGAGGTT CTTAACCTCG GTTAGTTAAG AACGGCCTCT GACACTTACG

2601 GCAAACCAAC CCTTGGCAGA ACATATCCAT GCCGCACGCG ATCTCCAGCA CGGCTCCGCC GGCAGCGTTG GGTCCTGGCC ACGGGTGCGC
     CGTTTGGTTG GGAACCGTCT TGTATAGGTA CGGCGTGCGC TAGAGGTCGT GCCGAGGCGG CCGTCGCAAC CCAGGACCGG TGCCCACGCG

2701 ATGATCGTGC TCCTGTCGTT GAGGACCCGG CTAGGCTGGC GGGGTTGCCT TACTGGTTAG CAGAATGAAT CACCGATACG TGAAGCGACT
     TACTAGCACG AGGACAGCAA CTCCTGGGCC GATCCGACCG CCCCAACGGA ATGACCAATC GTCTTACTTA GTGGCTATGC ACTTCGCTGA

2801 GCTGCTGCAA AACGTCTGCG ACCTGAGCAA CAACATGAAT GGTCTTCGGT TTCCGTGTTT CGTAAAGTCT GGAAACGCGG AAGTCAGCGC CCTGCACCAT
     CGACGACGTT TTGCAGACGC TGGACTCGTT GTTGTACTTA CCAGAAGCCA AAGGCACAAA GCATTCAGA CCTTTGCGCC TTCAGTCGCG GGACGTGGTA

2901 TATGTTCCGG ATCTGCATCG CAGGATGCTG CTGGCTACCC TGTGGAACAC CTACATCTGT ATTAACGAAG GACCCTGAGT GATTTTTCTC
     ATACAAGGCC TAGACGTAGC GTCCTACGAC GACCGATGGG ACACCTTGTG GATGTAGACA TAATTGCTTC CTGGGACTCA CTAAAAAGAG

3001 TGGTCCCGCC CGCCAGTTGT TTACCCTCAC CCCATGAACA GAAATTCCCC AACGTTCCAG TGTTCATCAT CAGTAACCCG ATCCTCTCTC
     ACCAGGGCGG GCGGTCAACA AATGGGAGTG GGGTACTTGT CTTTAAGGGG TTGCAAGGTC GTCATTGGTA GTCATTGGGC TAGGAGAGAG

3101 GTTTCATCGG TATCATTACC CCCATGAACA GAAATTCCCC AAACTCAACG CCTTAACAT CAGTAACCCG GAAAAAACCG CCCTTAACAT ATCGTGAGC
     CAAAGTAGCC ATAGTAATGG GGGTACTTGT CTTTAAGGGG TTTGAGTTGC GGAATTGTA GTCATTGGGC CTTTTTGGC GGGAATTGTA TAGGAGAGC

3201 ATCAGAAGCC AGACATTAAC GCTTCTGGAG AAACTCAACG GGCATCAAGT GGATGAACAG GCAGACATCT GTGAATCGCT TCACGACCAC GCTGATGAGC
     TAGTCTTCGG TCTGTAATTG CGAAGACCTC TTTGAGTTGC CCGTAGTTCA CCTACTTGTC CGTCTGTAGA CACTTAGCGA AGTGCTGGTG CGACTACTCG

3301 TTTACCGCAG GATCCGGAAA TTGTAAACGT TAATATATTTG CGTTAAATTT TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC
     AAATGGCGTC CTAGGCCTTT AACATTGCA ATTATAAAAC GCAATTTAAA AACAATTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG

3401 GGCAAAATCC CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG
     CCGTTTAGG GAATATTTAG TTTCTTATC TGGCTCTATC CCAACTCACA ACCTTGTCAA CAGGTGATAA TTTCTTGCAC CTGAGGTTGC

3501 TCAAAGGGGCG AAAAACCGTC TATCAGGGCT ATGGCCCACT ACGTGAACCA TCACCCTAAT CAAGTTTTTT GGGGTCGAGG CACTAAATCG
     AGTTCCCCGC TTTTGGCAG ATAGTCCCGA TACCGGGTGA TGCACTTGGT AGTGGGGATTA GTTCAAAAAA CCCCAGCTCC GTGATTTAGC

3601 GAACCCTAAA GGGAGCCCCC GATTTAGAGC TTGACGGGGA ACGTGGCGAG AAAGGAAGGA AAGGAAGCGA TGCCGTAAAG CGCTAGGCGG
     CTTGGGATTT CCCTCGGGGG CTAAATCTCG AACTGCCCCT TGCACCGCTC TTTCCTTCCC TTCCTTCGCT ACGGCATTTC GCGATCCCGC

3701 CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA ACCACCACAC CGCCCGCGCT TAATGCGGCT CGTCCTCGCG CGTTTCGGTG
     GACCGTTCAC ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GGCGGGCGCGA ATTACGCGGA GCAGGCCTAG GCAAAGCCAC

3801 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTCACAGCT TGTCTGTAAG CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGGTCAGC
     TACTGCCACT TTTGGAGACT GTGTACGTCG AGGGCCTCTG CCAGTGTCGA ACAGACATTC GCCTACGGCC CTCGTCTGTT CGGCAGTCC CGGCAGTCG
```

Fig. 8C

```
3901  GGTGTTGGC  GGGTGTCGGG  GCGCAGCCAT  GACCCAGTCA  CGTAGCGATA  GCGGAGTGTA  TACTGGCTTA  ACTATGGCGC  ATCAGAGCAG  ATTGTACTGA
      CCCACACCG  CCCACAGCCC  CGCGTCGGTA  CTGGGTCAGT  GCATCGCTAT  CGCCTCACAT  ATGACCGAAT  TGATACGCCG  TAGTCTCGTC  TAACATGACT

4001  GAGTGCACCA  TATGCGGTGT  GAAATACCGC  ACAGATGCGT  AAGGAGAAAA  TACCGCATCA  GGCGCTCTTC  CTCACTGACT  CGCTGCGCTC
      CTCACGTGGT  ATACGCCACA  CTTTATGGCG  TGTCTACGCA  TTCCTCTTTT  ATGGCGTAGT  CCGCGAGAAG  GAGTGACTGA  GCGACGCGAG

4101  GGTCGTTCGG  CTGCGGCGAG  CGGTATCAGC  TCACTCAAAG  GCGGTAATAC  GGTTATCCAC  AGAATCAGGG  GATAACGCAG  GTGAGCAAAA
      CCAGCAAGCC  GACGCCGCTC  GCCATAGTCG  AGTGAGTTTC  CGCCATTATG  CCAATAGGTG  TCTTAGTCCC  CTATTGCGTC  CACTCGTTTT

4201  GGCCAGCAAA  AGGCCAGGAA  CCGTAAAAAG  GCCGCGTTGC  GCGGCGTTTT  CCATAGGCTC  CGCCCCCCTG  ACGAGCATCA  CAAAAATCGA  CGCTCAGTC
      CCGGTCGTTT  TCCGGTCCTT  GGCATTTTTC  CGGCGCAACG  CGCCCAACGG  GGTATCCCAG  GCGGGGGGAC  TGCTCGTAGT  GTTTTTAGCT  GCGAGTTCAG

4301  AGAGGTGGCG  AAACCCGACA  GGACTATAAA  GATACCAGGC  GTTTCCCCCT  GGAAGCTCCC  TCGTGCGCTC  ACCCTGCCGC  TTACCGGATA
      TCTCCACCGC  TTTGGGCTGT  CCTGATATTT  CTATGGTCCG  CAAAGGGGGA  CCTTCGAGGG  AGCACGCGAG  TGGGACGGCG  AATGGCCTAT

4401  CCTGTCCGCC  TTTCTCCCTT  CGGGAAGCGT  GGCGCTTTCT  CATAGCTCAC  GCTGTAGGTA  TCTCAGTTCG  GTGTAGGTCG  TTCGCTCCAA  GCTGGGCTGT
      GGACAGGCGG  AAAGAGGGAA  GCCCTTCGCA  CCGCGAAAGA  GTATCGAGTG  CGACATCCAT  AGAGTCAAGC  CACATCCAGC  AAGCGAGGTT  CGACCCGACA

4501  GTGCACGAAC  CCCCCGTTCA  GCCCGACCGC  TGCGCCTTAT  CCGGTAACTA  TCGTCTTGAG  TCCAACCCGG  TAAGACACGA  CTTATCGCCA  CTGGCAGCAG
      CACGTGCTTG  GGGGGCAAGT  CGGGCTGGCG  ACGCGGAATA  GGCCATTGAT  AGCAGAACTC  AGGTTGGGCC  ATTCTGTGCT  GAATAGCGGT  GACCGTCGTC

4601  CCACTGGTAA  CAGGATTAGC  AGAGCGAGGT  ATGTAGGCGG  TGCTACAGAG  TTCTTGAAGT  GGTGGCCTAA  CTACGGCTAC  ACTAGAAGGA  CAGTATTTGG
      GGTGACCATT  GTCCTAATCG  TCTCGCTCCA  TACATCCGCC  ACGATGTCTC  AAGAACTTCA  CCACCGGATT  GATGCCGATG  TGATCTTCCT  GTCATAAACC

4701  TATCTGCGCT  CTGCTGAAGC  CAGTTACCTT  CGGAAAAAGA  GTTGGTAGCT  CTTGATCCGG  CAAACAAACC  ACCGCTGGTA  GCGGTGGTTT  TTTTGTTTGC
      ATAGACGCGA  GACGACTTCG  GTCAATGGAA  GCCTTTTTCT  CAACCATCGA  GAACTAGGCC  GTTTGTTTGG  TGGCGACCAT  CGCCACCAAA  AAAACAAACG

4801  AAGCAGCAGA  TTACGCGCAG  AAAAAAAGGA  TCTCAAGAAG  ATCCTTTGAT  CTTTTCTACG  GGGTCTGACG  CTCAGTGGAA  CGAAAACTCA  CGTTAAGGGA
      TTCGTCGTCT  AATGCGCGTC  TTTTTTTCCT  AGAGTTCTTC  TAGGAAACTA  GAAAGATGC   CCCAGACTGC  GAGTCACCTT  GCTTTTGAGT  GCAATTCCCT

4901  TTTTGGTCAT  GAGATTATCA  AAAAGGATCT  TCACCTAGAT  CCTTTTAAAT  TAAAAATGAA  GTTTTAAATC  AATCTAAAGT  ATATATGAGT  AAACTTGGTC
      AAAACCAGTA  CTCTAATAGT  TTTTCCTAGA  AGTGGATCTA  GGAAAATTTA  ATTTTTACTT  CAAAATTTAG  TTAGATTTCA  TATATACTCA  TTTGAACCAG

5001  TGACAGTTAC  CAATGCTTAA  TCAGTGAGGC  ACCTATCTCA  GCGATCTGTC  TATTTCGTTC  ATCCATAGTT  GCCTGACTCC  CCGTCGTGTA  GATAACTACG
      ACTGTCAATG  GTTACGAATT  AGTCACTCCG  TGGATAGAGT  CGCTAGACAG  ATAAAGCAAG  TAGGTATCAA  CGGACTGAGG  GGCAGCACAT  CTATTGATGC

5101  ATACGGGAGG  GCTTACCATC  TGGCCCCAGT  GCTGCAATGA  TACCGCGAGA  CCCACGCTCA  CCGGCTCCAG  ATTTATCAGC  AATAAACCAG  CCAGCCGGAA
      TATGCCCTCC  CGAATGGTAG  ACCGGGGTCA  CGACGTTACT  ATGGCGCTCT  GGGTGCGAGT  GGCCGAGGTC  TAAATAGTCG  TTATTTGGTC  GGTCGGCCTT

5201  GGGCCGAGCG  CAGAAGTGGT  CCTGCAACTT  TATCCGCCTC  CATCCAGTCT  ATTAATTGTT  GCCGGGAAGC  TAGAGTAAGT  AGTTCGCCAG  TTAATAGTTT
      CCCGGCTCGC  GTCTTCACCA  GGACGTTGAA  ATAGGCGGAG  GTAGGTCAGA  TAATTAACAA  CGGCCCTTCG  ATCTCATTCA  TCAAGCGGTC  AATTATCAAA

5301  GCGCAACGTT  GTTGCCATTG  CTGCAGGCAT  CGTGGTGTCA  CGCTCGTCGT  TTGGTATGGC  TTCATTCAGC  TCCGGTTCCC  AACGATCAAG  GCGAGTTACA
      CGCGTTGCAA  CAACGGTAAC  GACGTCCGTA  GCACCACAGT  GCGAGCAGCA  AACCATACCG  AAGTAAGTCG  AGGCCAAGGG  TTGCTAGTTC  CGCTCAATGT

5401  TGATCCCCCA  TGTTGTGCAA  AAAAGCGGTT  AGCTCCTTCG  GTCCTCCGAT  CGTTGTCAGA  AGTAAGTTGG  CCGCAGTGTT  ATCACTCATG  GTTATGGCAG
      ACTAGGGGGT  ACAACACGTT  TTTTCGCCAA  TCGAGGAAGC  CAGGAGGCTA  GCAACAGTCT  TCATTCAACC  GGCGTCACAA  TAGTGAGTAC  CAATACCGTC

5501  CACTGCATAA  TTCTCTTACT  GTCATGCCAT  CCGTAAGATG  CTTTTCTGTG  ACTGGTGAGT  ACTCAACCAA  GTCATTCTGA  GAATAGTGTA  TGCGGCGACC
      GTGACGTATT  AAGAGAATGA  CAGTACGGTA  GGCATTCTAC  GAAAAGACAC  TGACCACTCA  TGAGTTGGTT  CAGTAAGACT  CTTATCACAT  ACGCCGCTGG
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Fig. 8D

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5601 GAGTTGCTCT TGCCCGGCGT CAACACGGGA TAATACCGGG CCAACATAGCA GAACTATAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC
     CTCAACGAGA ACGGGCCGCA GTTGTGCCCT ATTATGGCGC GGTGTATCGT CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG

5701 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG
     AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCACG TGGGTTGACT AGAAGTCGTA GAAAATGAAA GTGGTCGCAA AGACCCACTC

5801 CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA
     GTTTTTGTCC TTCCGTTTTA CGGCGTTTTT TCCCTTATTC CCGCTGTGCC TTTACAACTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT

5901 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG CGCACATTTC CCCGAAAAGT GCCACCTGAC
     AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA TAAATCTTTT TATTTGTTTA TCCCCAAGGC GCGTGTAAAG GGGCTTTTCA CGGTGGACTG

6001 GTCTAAGAAA CCATTATTAT CATGACATTA ACCTATAAAA ATAGGCGTAT CACGAGGCCC TTTCGTCTTC AA (SEQ ID NO: 99)
     CAGATTCTTT GGTAATAATA GTACTGTAAT TGGATATTTT TATCCGCATA GTGCTCCGGG AAAGCAGAAG TT
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Fig. 8E

■ = differences from F(ab)-12

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                  10            20            30
F(ab)-12 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
MB1.6    DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
H2305.6  DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
Y0101    DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
Y0192    DIQ■TQSPSSLSASVGDRVTITC■■■■■■SNYLNWYQQ
                                    CDR-L1
         40            50            60        70
F(ab)-12 KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
MB1.6    KPGKAPK■■LIYFTSSLHSGVPSRFSGSGSGTD■TLTIS
H2305.6  KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTD■TLTIS          Fig. 9A
Y0101    KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
Y0192    KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
                CDR-L2
              80          90            100
F(ab)-12 SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:8)
MB1.6    SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 101)
H2305.6  SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:103)
Y0101    SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:105)
Y0192    SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 107)
                         CDR-L3
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                  10            20            30
F(ab)-12 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR
MB1.6    EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNW■R
H2305.6  EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNW■R
Y0101    EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR
Y0192    EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYG■NWVR
                                      CDR-H1
         40            50            60        70
F(ab)-12 QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
MB1.6    QAPGKGLEWVGWINTYTGEPTYAADFKRRFT■■ADTS■■■■
H2305.6  QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFS■DTS■■■■      Fig. 9B
Y0101    QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
Y0192    QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
                CDR-H2                       CDR-7
         80          90          100          110
F(ab)-12 YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:7)
MB1.6    YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:102)
H2305.6  YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO: 104)
Y0101    YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:106)
Y0192    YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:108)
                         CDR-H3
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                10             20             30
F(ab)-12  DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
Y0243-1   DIQ■TQSPSSLSASVGDRVTITCRANEOLSNYLNWYQQ
Y0238-3   DIQ■TQSPSSLSASVGDRVTITCRANEOLSNYLNWYQQ
Y0313-1   DIQ■TQSPSSLSASVGDRVTITCRANEOLSNYLNWYQQ
Y0317     DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ
                                          CDR-L1
          40             50             60        70
F(ab)-12  KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
Y0243-1   KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
Y0238-3   KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS      Fig. 10A
Y0313-1   KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
Y0317     KPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTIS
               CDR-L2
              80      CDR-L2 90          100
F(ab)-12  SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:8)
Y0243-1   SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:109)
Y0238-3   SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:111)
Y0313-1   SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:113)
Y0317     SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO:115)
                  CDR-L3
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                10             20             30
F(ab)-12  EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR
Y0243-1   EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR
Y0238-3   EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYG■NWVR
Y0313-1   EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR
Y0317     EVQLVESGGGLVQPGGSLRLSCAASGY■FT■YGMNWVR
                                          CDR-H1
          40             50             60        70
F(ab)-12  QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
Y0243-1   QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
Y0238-3   QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA   Fig. 10B
Y0313-1   QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
Y0317     QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA
               CDR-H2                             CDR-7
          80           90    100          110
F(ab)-12  YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:7)
Y0243-1   YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTL (SEQ ID NO:110)
Y0238-3   YLQMNSLRAEDTAVYYCAKYP■YYG■SHWYFDVWGQGTL (SEQ ID NO:112)
Y0313-1   YLQMNSLRAEDTAVYYCAKYP■YYG■SHWYFDVWGQGTL (SEQ ID NO:114)
Y0317     YLQMNSLRAEDTAVYYCAKYP■YYG■SHWYFDVWGQGTL (SEQ ID NO:116)
                           CDR-H3
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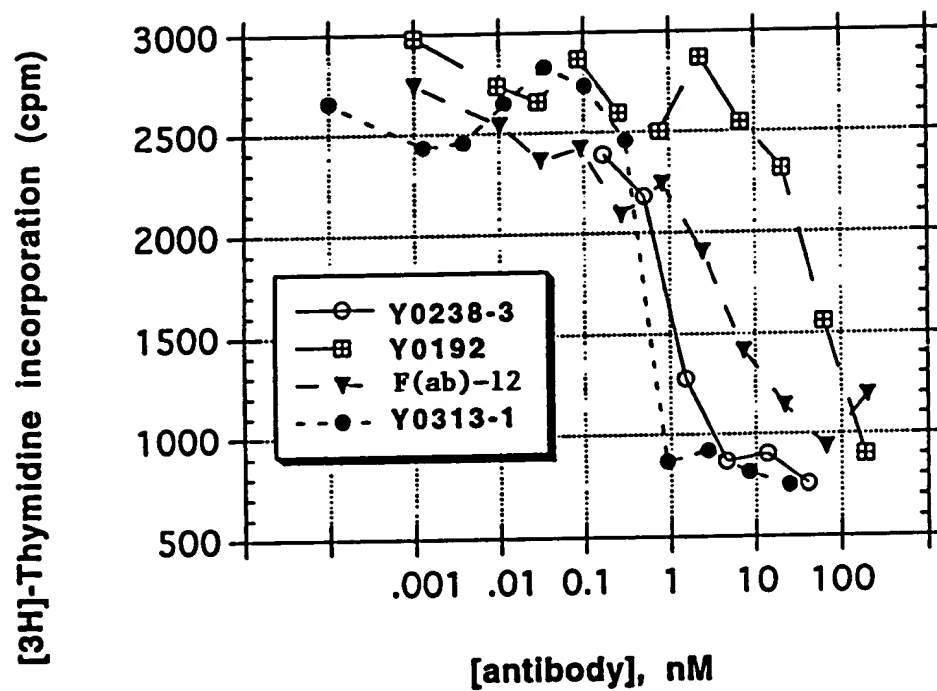
Fig. 11

Fig. 12